



#7

## SEQUENCE LISTING

<110> Darrow, Andrew  
Qi, Jenson  
Andrade-Grodon, Patricia

<120> Zymogen Activation System

<130> ORT-1552

<140> 10/015,989

<141> 2001-12-10

<150> 09/303,162

<151> 1999-04-30

<160> 60

<170> PatentIn version 3.2.

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<223> Fusion Gene Vectors

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atacattgat gagtttggac aaaccacaac tagaatgcag tgaaaaaaat gctttatttg 300  
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 ccgattacgc ctagcggccg cttcccttta gtgaggggta atgcttcgag cagacatgat 360  
 aagatacatt gatgagtttg gacaaaccac aactagaatg cagtgaaaaa aatgctttat 420  
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 gcttcgagca gacatgataa gatacattga tgagtttgga caaaccacaa ctagaatgca 300  
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agcggccgct tccctttagt gagggttaat gcttcgagca gacatgataa gatacattga	240
tgagtttgga caaaccacaa ctagaatgca gtgaaaaaaaa tgctttattt gtgaaatttg	300
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gaatgcagtg aaaaaaatgc tttatttgtg aaatttgtga tgctattgct ttatttgtaa	1140
ccattataag ctgcaataaa caagttgac	1169

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Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys  
 20 25 30

Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp  
 35 40 45

Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Ala Gly Gln Trp Pro  
 50 55 60

Trp Gln Val Ser Ile Thr Tyr Glu Gly Val His Val Cys Gly Gly Ser  
 65 70 75 80

Leu Val Ser Glu Gln Trp Val Leu Ser Ala Ala His Cys Phe Pro Ser  
85 90 95

Glu His His Lys Glu Ala Tyr Glu Val Lys Leu Gly Ala His Gln Leu  
100 105 110

Asp Ser Tyr Ser Glu Asp Ala Lys Val Ser Thr Leu Lys Asp Ile Ile  
115 120 125

Pro His Pro Ser Tyr Leu Gln Glu Gly Ser Gln Gly Asp Ile Ala Leu  
130 135 140

Leu Gln Leu Ser Arg Pro Ile Thr Phe Ser Arg Tyr Ile Arg Pro Ile  
145 150 155 160

Cys Leu Pro Ala Ala Asn Ala Ser Phe Pro Asn Gly Leu His Cys Thr  
165 170 175

Val Thr Gly Trp Gly His Val Ala Pro Ser Val Ser Leu Leu Thr Pro  
180 185 190

Lys Pro Leu Gln Gln Leu Glu Val Pro Leu Ile Ser Arg Glu Thr Cys  
195 200 205

Asn Cys Leu Tyr Asn Ile Asp Ala Lys Pro Glu Glu Pro His Phe Val  
210 215 220

Gln Glu Asp Met Val Cys Ala Gly Tyr Val Glu Gly Gly Lys Asp Ala  
225 230 235 240

Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Cys Pro Val Glu Gly Leu  
245 250 255

Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Asp Ala Cys Gly Ala Arg  
260 265 270

Asn Arg Pro Gly Val Tyr Thr Leu Ala Ser Ser Tyr Ala Ser Trp Ile  
275 280 285

Gln Ser Lys Val Thr Glu Leu Gln Pro Arg Val Val Pro Gln Thr Gln  
290 295 300

Glu Ser Gln Pro Asp Ser Asn Leu Cys Gly Ser His Leu Ala Phe Ser  
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Ser Arg His His His His His His  
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 35 40 45

Leu Glu Ala Gly Gln Trp Pro Trp Gln Val Ser Ile Thr Tyr Glu Gly  
 50 55 60

Val His Val Cys Gly Gly Ser Leu Val Ser Glu Gln Trp Val Leu Ser  
 65 70 75 80

Ala Ala His Cys Phe Pro Ser Glu His His Lys Glu Ala Tyr Glu Val  
 85 90 95

Lys Leu Gly Ala His Gln Leu Asp Ser Tyr Ser Glu Asp Ala Lys Val  
 100 105 110

Ser Thr Leu Lys Asp Ile Ile Pro His Pro Ser Tyr Leu Gln Glu Gly  
 115 120 125

Ser Gln Gly Asp Ile Ala Leu Leu Gln Leu Ser Arg Pro Ile Thr Phe  
 130 135 140

Ser Arg Tyr Ile Arg Pro Ile Cys Leu Pro Ala Ala Asn Ala Ser Phe  
 145 150 155 160

Pro Asn Gly Leu His Cys Thr Val Thr Gly Trp Gly His Val Ala Pro  
 165 170 175

Ser Val Ser Leu Leu Thr Pro Lys Pro Leu Gln Gln Leu Glu Val Pro  
 180 185 190

Leu Ile Ser Arg Glu Thr Cys Asn Cys Leu Tyr Asn Ile Asp Ala Lys  
 195 200 205



Pro Glu Glu Pro His Phe Val Gln Glu Asp Met Val Cys Ala Gly Tyr  
210 215 220

Val Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu  
225 230 235 240

Ser Cys Pro Val Glu Gly Leu Trp Tyr Leu Thr Gly Ile Val Ser Trp  
245 250 255

Gly Asp Ala Cys Gly Ala Arg Asn Arg Pro Gly Val Tyr Thr Leu Ala  
260 265 270

Ser Ser Tyr Ala Ser Trp Ile Gln Ser Lys Val Thr Glu Leu Gln Pro  
275 280 285

Arg Val Val Pro Gln Thr Gln Glu Ser Gln Pro Asp Ser Asn Leu Cys  
290 295 300

Gly Ser His Leu Ala Phe Ser Ser Arg His His His His His His  
305 310 315

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Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu Leu  
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Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys  
20 25 30

Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp  
35 40 45

Asp Asp Lys Ile Val Gly Gly Tyr Asn Cys Leu Glu Pro His Ser Gln  
50 55 60

Pro Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly  
65 70 75 80

Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys Lys  
85 90 95

Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn Lys Asp  
100 105 110

Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro His Pro Cys  
115 120 125

Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp Leu Met Leu Leu  
130 135 140

Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys Val Lys Pro Ile Ser  
145 150 155 160

Leu Ala Asp His Cys Thr Gln Pro Gly Gln Lys Cys Thr Val Ser Gly  
165 170 175

Trp Gly Thr Val Thr Ser Pro Arg Glu Asn Phe Pro Asp Thr Leu Asn  
180 185 190

Cys Ala Glu Val Lys Ile Phe Pro Gln Lys Lys Cys Glu Asp Ala Tyr  
195 200 205

Pro Gly Gln Ile Thr Asp Gly Met Val Cys Ala Gly Ser Ser Lys Gly  
210 215 220

Ala Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asp Gly  
225 230 235 240

Ala Leu Gln Gly Ile Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser  
245 250 255

Asp Lys Pro Gly Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile  
260 265 270

Lys Lys Ile Ile Gly Ser Lys Gly Ser Arg His His His His His His  
275 280 285

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Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp  
 35 40 45

Asp Asp Lys Ile Val Gly Gly Tyr Asn Cys Leu Glu Lys His Ser Gln  
 50 55 60

Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala  
 65 70 75 80

Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys  
 85 90 95

Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu Glu  
 100 105 110

Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly  
 115 120 125

Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu  
 130 135 140

Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu  
 145 150 155 160

Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser  
 165 170 175

Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu  
 180 185 190

Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala  
 195 200 205

Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu  
 210 215 220

Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
 225 230 235 240

Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala  
 245 250 255

Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val Asp  
 260 265 270

Trp Ile Gln Glu Thr Met Lys Asn Asn Ser Arg His His His His His  
 275 280 285

His

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ctagatagc

9

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9

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<210> 29  
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<400> 35  
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47

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53

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28

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 <220>  
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<210> 47  
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<400> 47  
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<210> 48  
<211> 28  
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<400> 48  
gctggtctag agctgaaggc caggtggc 28

<210> 49  
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<212> DNA  
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<400> 49  
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<210> 50  
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<400> 50  
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<210> 51  
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<400> 51  
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<210> 52  
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<400> 52  
gtcctctaga attgttcttc atcgtctcct gg

32

<210> 53  
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<220>  
<223> Fusion Gene Of Human Protease F In CFEK2 Zymogen Vector

<400> 53

Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr  
1 5 10 15

Phe Gly Cys Gly Val Pro Asp Tyr Lys Asp Asp Asp Asp Ala Ala Ala  
20 25 30

Leu Ala Ala Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Ala  
35 40 45

Leu Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp  
50 55 60

Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr  
65 70 75 80

Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu Ser Asp Pro Ser Gly  
85 90 95

Trp Met Val Gln Phe Gly Gln Leu Thr Ser Met Pro Ser Phe Trp Ser  
100 105 110

Leu Gln Ala Tyr Tyr Asn Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser  
115 120 125

Pro Arg Tyr Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu  
130 135 140

Ser Ala Pro Val Thr Tyr Thr Lys His Ile Gln Pro Ile Cys Leu Gln  
145 150 155 160

Ala Ser Thr Phe Glu Phe Glu Asn Arg Thr Asp Cys Trp Val Thr Gly  
165 170 175

Trp Gly Tyr Ile Lys Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu  
180 185 190

Gln Glu Val Gln Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu  
195 200 205

Phe Leu Lys Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys  
210 215 220

Ala Gly Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly  
225 230 235 240

Gly Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
245 250 255

Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr  
260 265 270

Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met Ala Gln  
275 280 285

Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Ser Arg His His His His  
290 295 300

His His  
305

<210> 54  
<211> 284  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human MH2 Protease In PFEK Zymogen Vector  
<400> 54

Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu Leu  
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Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys  
20 25 30

Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp  
35 40 45

Asp Asp Lys Ile Val Gly Gly Tyr Asn Cys Leu Glu Pro His Ser Gln  
50 55 60

Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu Phe Cys Ser Gly  
65 70 75 80

Val Leu Val His Pro Gln Trp Val Leu Ser Ala Ala His Cys Phe Gln  
85 90 95

Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu Glu Ala Asp Gln  
100 105 110

Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu Ser Val Arg His Pro  
115 120 125

Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu  
130 135 140

Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala  
145 150 155 160

Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly  
165 170 175

Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys Val Asn Val  
180 185 190

Ser Val Val Ser Glu Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr  
195 200 205

His Pro Ser Met Phe Cys Ala Gly Gly Gly His Asp Gln Lys Asp Ser  
210 215 220

Cys Asn Gly Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln  
225 230 235 240

Gly Leu Val Ser Phe Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro  
245 250 255

Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr  
260 265 270

Val Gln Ala Ser Ser Arg His His His His His His  
275 280

<210> 55  
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<400> 55  
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<210> 56  
<211> 30  
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<220>  
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<400> 56  
cccatctaga actggcctgg acggttttct 30

<210> 57  
<211> 32  
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<220>  
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<400> 57  
aggatctaga actcgggcgt tggccgtggc ag 32

<210> 58  
<211> 30  
<212> DNA  
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<220>  
<223> PCR Primer

<400> 58  
agagtctaga ccaggagggg tctggctggg 30

<210> 59  
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<212> DNA  
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<220>  
<223> Nucleic Acid Sequence Of Human Protease F In CFEK2 Zymogen Vector

<400> 59  
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ttcggctgcg ggggtccccga ctacaaggac gacgacgacg cggccgctct tgctgcccc 120  
tttgatgatg atgacaagat cggtgggggc tatgctctag aactcgggcg ttggccgtgg 180  
caggggagcc tgcgcctgtg ggattccac gtatgcggag tgagcctgct cagccaccgc 240  
tgggcactca cggcggcgca ctgctttgaa acctatagt accttagtga tccctccggg 300  
tggatggtcc agtttgcca gctgacttcc atgccatcct tctggagcct gcaggcctac 360  
tacaaccgtt acttcgtatc gaatatctat ctgagccctc gctacctggg gaattcacc 420  
tatgacattg ccttggtgaa gctgtctgca cctgtcacct acactaaaca catccagccc 480

atctgtctcc aggcctccac atttgagttt gagaaccgga cagactgctg ggtgactggc	540
tgggggtaca tcaaagagga tgaggcactg ccatctcccc acaccctcca ggaagttcag	600
gtcgccatca taaacaactc tatgtgcaac cacctcttcc tcaagtacag tttccgcaag	660
gacatctttg gagacatggt ttgtgctggc aatgccaag gcgggaagga tgcctgcttc	720
ggtgactcag gtggaccctt ggcctgtaac aagaatggac tgtggatatca gattggagtc	780
gtgagctggg gagtgggctg tggtcggccc aatcggcccg gtgtctacac caatatcagc	840
caccactttg agtggatcca gaagctgatg gccagagtg gcatgtccca gccagacccc	900
tcctgggtcta gacatcacca tcaccatcac tagcggccgc ttccctttag tgaggggtaa	960
tgcttcgagc agacatgata agatacattg atgagtttgg acaaaccaca actagaatgc	1020
agtgaaaaaa atgctttatt tgtgaaattt gtgatgctat tgctttattt gtaaccatta	1080
taagctgcaa taaacaagtt gac	1103

<210> 60

<211> 1037

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic Acid Sequence Of Human MH2 Protease In PFEK Zymogen Vector

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gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctac	180
aactgtctag agccgcactc gcagccctgg caggcggcac tggatcatgga aaacgaattg	240
ttctgctcgg gcgtcctggt gcatccgcag tgggtgctgt cagccgcaca ctgtttccag	300
aactcctaca ccatcgggct gggcctgcac agtcttgagg ccgaccaaga gccagggagc	360
cagatggtgg aggccagcct ctccgtacgg caccagagat acaacagacc cttgctcgct	420
aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc	480
atcagcattg cttcgcagtg ccctaccgcg gggaaactct gcctcgtttc tggctggggg	540
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gaggaggtct gcagtaagct ctatgacccg ctgtaccacc ccagcatggt ctgcgccggc	660
ggagggcacg accagaagga ctcttgaac ggtgactctg gggggcccct gatctgcaac	720
gggtacttgc agggccttgt gtctttcgga aaagccccgt gtggccaagt tggcgtgcc	780
ggtgtctaca ccaacctctg caaattcact gagtggatag agaaaaccgt ccaggccagt	840
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gcaataaaca agttgac 1037